

1	AGCAGACAGAGGACTCTCATTAAGGAAG	TGCTGTGCTGCCCTGACCTACAAGATGCCA	AGAGAGATGCTCAGCTTCATCTATGTTTAC	CCCAAGAGGGGACGGCCACTCTTACACC	119
120	ThraLeGluGluAlaAlaGlyLleGlyLle	LeuThrValLleLeuGluValLeuLeuLeu	ATCGCTGTTGCTTATTCTAGACGCAAT	GGATACAGAGCCTTTCATGATATAAGTCTT	22
23	ThraLeGluGluAlaAlaGlyLleGlyLle	LeuThrValLleLeuGluValLeuLeuLeu	ATCGCTGTTGCTTATTCTAGACGCAAT	GGATACAGAGCCTTTCATGATATAAGTCTT	239
240	CATGTTGGCACTCAATGTGCTTAAACAGA	AGATGCCACACAGAGGCTTTCATCATCGG	GACAGCAAGTGTCTCTTCAAGAGAAAAC	TGTGAACCTGTGCTTCCCAATGCTCCACCT	62
63	HisValGlyThrGlnCysAlaLeuThrArg	ArgCysProGlnGluGlyPheLeuHisArg	AspSerLeuValSerLeuGlnGluLeuVal	CysGluProValValProAlaAlaProPro	359
360	GCTTATGAGAACTCTCTGAGAACAGTCA	CCACCACCTTATTACCTTAAAGCCAGCG	AGACACCTGAGACATGCTGMAATTATTCT	CTCACACTTTTCTGCTTGAATTTTAAACAGAC	102
103	AlaTyxGluLysLeuSerAlaGluGlnSer	ProProProTyxSerPro			479
480	ATCTAATGTTCTCTTGGAAATGCTGTAAG	AAAAATGCAAGCCATCTCTAATAATAAGTC	AGTGTAAATTTTATAGTCCGCTAGCA	GTACTAATCATGTGAGGAAATGATGAGAAA	118
600	TATTAAATGGGAAACTCCATCAATNAAT	GTTCGAATGCAATGATATCTCTGCCCAGA	GGTAAATGTAGTAAATCAATGCTGTTATTT	TCTGAGAGACAGAAATTCAGTGGGTATTCT	599
720	GGGCCCATCCAAATTTCTCTTACTTGAAT	TTGGCTAATAACAACTAGTCAAGATTTTCG	AACCTTGACCAATGAACTGTACACAGAA	TTGTTCCAGTACTATGAGTGTCTCAAAAG	719
840	GATACCTTTACAGGTTTAAAGCAAGGGTTG	ACTGGCTATTATCTGATCAAGACATGT	CAGCAATGTCTCTTTGTGCTCTAATAATCT	ATTATACACATAATATATATTTAAAGATC	839
960	CTATAGCTCTTTTCTTGGATGAGGTTT	CCCTTTTGTGCTCCAGGCTGAGTGCATAG	GGCGATCTTGGCTCACCATAACCTCGCC	TCCAGGTTTCAAGCAATTTCTCTGCTTAG	959
1080	CTCTCTAGTACGTTGATTTACAGGCTGCG	GGCACTATGCTGCTGACTAATTTGTAGTTT	GGATCTATATCTTAGGTAAGACATATAC	GGCTGTCTTCAAACTCTGACCTCAGGTGA	1079
1200	TCTGCCCGCTCAGCTCCCAAGTGTGCG	AAATTACAGGCTGAGCCACCGCTGCTGCT	GGATCTATATCTTAGGTAAGACATATAC	GGCTGTCTTCAAACTCTGACCTCAGGTGA	1119
1320	AATGCTATTCTAATGACAAAGTATTTT	CTACTAAACCAAGAAATTTGTAAGGATTT	AAATAAGTAAAGCTACTATGTACTGCTCT	AGTGTGTATGCTGTGTACTGCTTAAATG	143
1440	TACCTATGCAATTTAGCTCTCTTGGGTTG	CCAAATCCCTCTCACAGAAATGTGCAGAG	AAATCATAAAGGATCAGAGATTTCTGAAAA	AAAAAAAATAAAAAATAAAAAATAAAAA	1559

FIGURE 1

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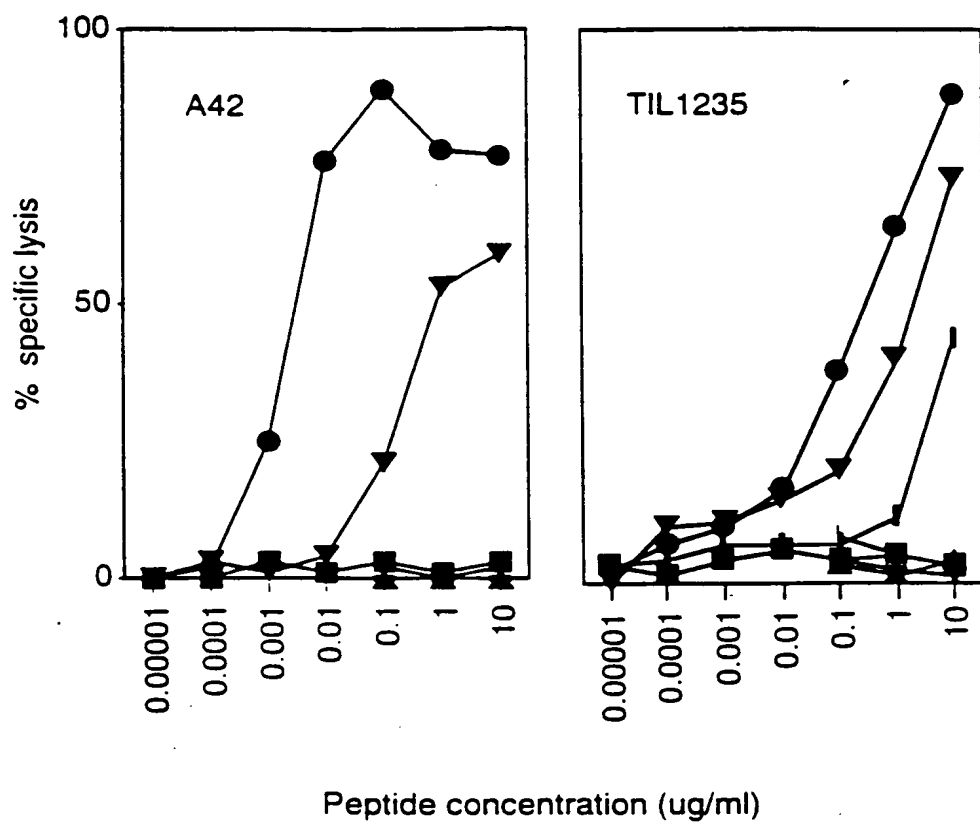


FIGURE 2

FIGURE 3A

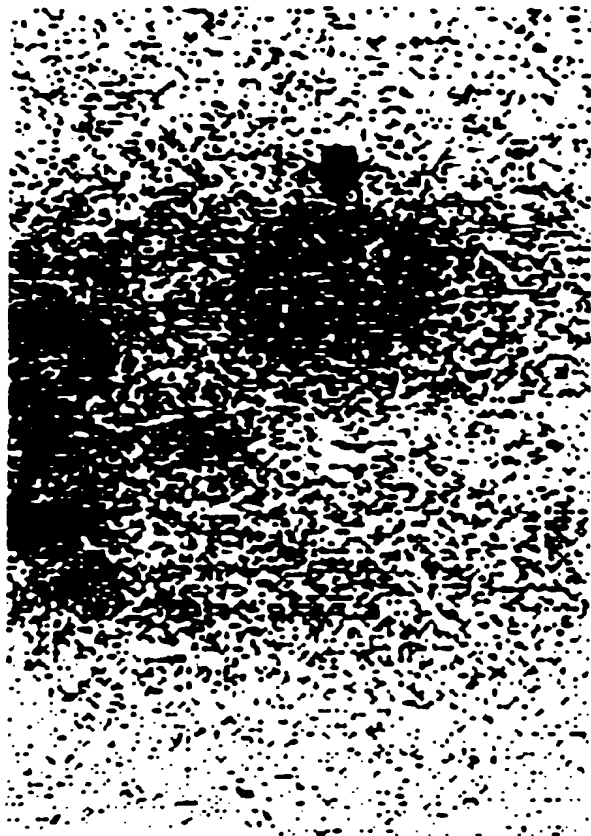
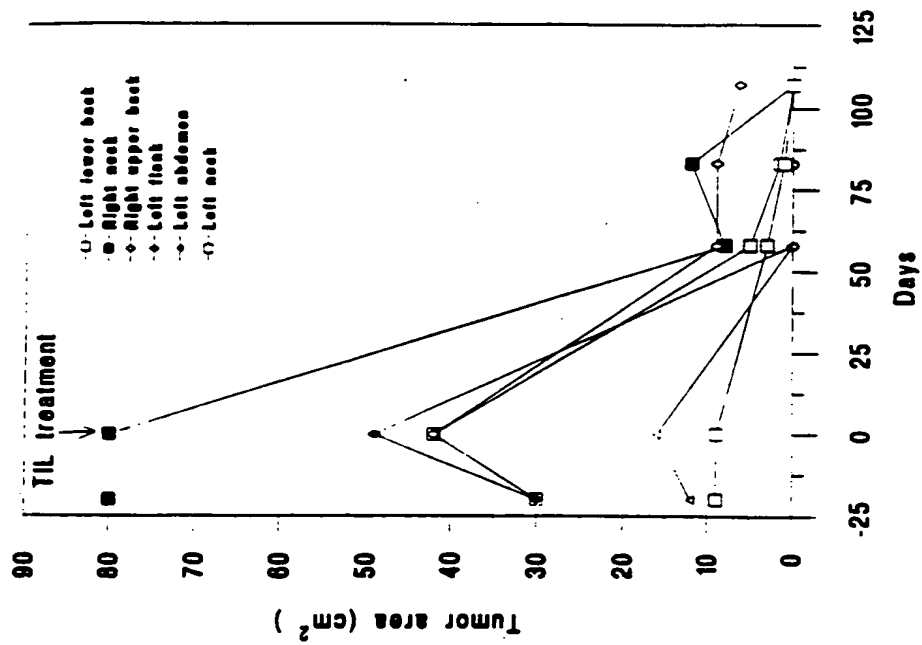


FIGURE 3B



GTCTGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT	40
GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG	80
ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA	120
GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC	160
CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA	200
GCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCC	240
TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAAA	280
TGCCTCCTTC TCTATTGCCT TGAACCTCCC TGGAAGCCAA	320
AAGGTATTGC CAGATGGGCA GGTTATCTGG GTCAACAATA	360
CCATCATCAA TGGGAGCCAG GTGTGGGGAG GACAGCCAGT	400
GTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT	440
GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA	480
GCTTTGTTTA TGTCTGGAAG ACCTGGGGCC AATACTGGCA	520
ATTTCTAGGG GGCCCAGTGT CTGGGCTGAG CATTGGGACA	560
GGCAGGGCAA TGCTGGGCAC ACACACCATG GAAGTGACTG	600
TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC	640
TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT	680
TTCTCCGTGA GCGTGTCCCA GTTGCGGGCC TTGGATGGAG	720
GGAACAAGCA CTTCTGAGA AATCAGCCTC TGACCTTTGC	760
CCTCCAGCTC CATGACCCCA GTGGCTATCT GGCTGAAGCT	800
GACCTCTCCT ACACCTGGGA CTTTGGAGAC AGTAGTGGAA	840
CCCTGATCTC TCGGGCACTT GTGGTCACTC ATACTTACCT	880
GGAGCCTGGC CCAGTCACTG CCCAGGTGGT CCTGCAGGCT	920
GCCATTCTC TCACCTCCTG TGGCTCCTCC CCAGTTCCAG	960
GCACCACAGA TGGGCACAGG CCAACTGCAG AGGCCCTTAA	1000
CACCACAGCT GGCCAAGTGC CTACTACAGA AGTTGTGGGT	1040
ACTACACCTG GTCAGGCGCC AACTGCAGAG CCCTCTGGAA	1080
CCACATCTGT GCAGGTGCCA ACCACTGAAG TCATAAGCAC	1120

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TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG	1160
ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA	1200
CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC	1240
ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAACCACA	1280
GCTGCACAGG TAACAACTAC AGAGTGGGTG GAGACCACAG	1320
CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC	1360
CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG	1400
GGCCCCCTGC TGGATGGTAC AGCCACCTTA AGGCTGGTGA	1440
AGAGACAAGT CCCCCTGGAT TGTGTTCTGT ATCGATATGG	1480
TTCCTTTTCC GTCACCCTGG ACATTGTCCA GGGTATTGAA	1520
AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG	1560
ATGCATTTGA GCTGACTGTG TCCTGCCAAG GCGGGCTGCC	1600
CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG	1640
CCCCCTGCCC AGCGGCTGTG CCAGCCTGTG CTACCCAGCC	1680
CAGCCTGCCA GCTGGTTCTG CACCAGATAC TGAAGGGTGG	1720
CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC	1760
AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG	1800
GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG	1840
CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG	1880
ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC	1920
CCCAGTTGCC ACATAGCAGC AGTCACTGGC TGCCTCTACC	1960
CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC	2000
CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG	2040
CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC	2080
CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT	2120
ACTCAGAGCC TGAAAAAAAA TAAAAAAAAA AAAAAAAAAA	2160
AAAAAAAAAA AA	2172

FIGURE 4 (continued)

FIGURE 5A

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1 MDLVLRCLL HLAIVIGALLA VGATKVPRNQ DWLGVSRLR TKAWNROLYP
51 EWTEAQRLLC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLDPG
101 QVIWVNNITII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV
151 YVWKTWGQYW QFLGGPVSGL SIGTGRAMLG THTMEVTVYH RRGSRSYVPL
201 AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNOPLTF ALQLHDPSGY
251 LAEADLSYTW DFGDSSGTLI SRALVVTHY LEPGPVTAQV VLQAAIPLTS
301 CGSSPVPGETT DGHRTAEAP NTTAGQVPTT EVVGTTPGOA PTAEPSGTTS
351 VQVPTTEVIS TAPVQMPAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM
401 TPAEVSIVVL SGTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI
451 TGSGLPLLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV OGIESAEILQ
501 AVPSGEGDAF ELTVSCQGL PKEACMEISS PGCOPPAQRL CQVLPSPAC
551 QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV
601 GILLVLMVV LASLIYRRRL MKQDFSVPOL PHSSSHWLRL PRIFCSCPIG
651 ENSPLLSGQQ V

```

FIGURE 5B

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Pme117 M-----V-----Q-----P-----VPGILLT-----LLSGQQV
ME20 M-----V-----Q-----L-----
gp100 M-----V-----Q-----L-----
cDNA25FL M-----F-----Q-----L-----
cDNA25TR Q-----L-----PPQWAAGLSTLI
1 162 236 274 588 649

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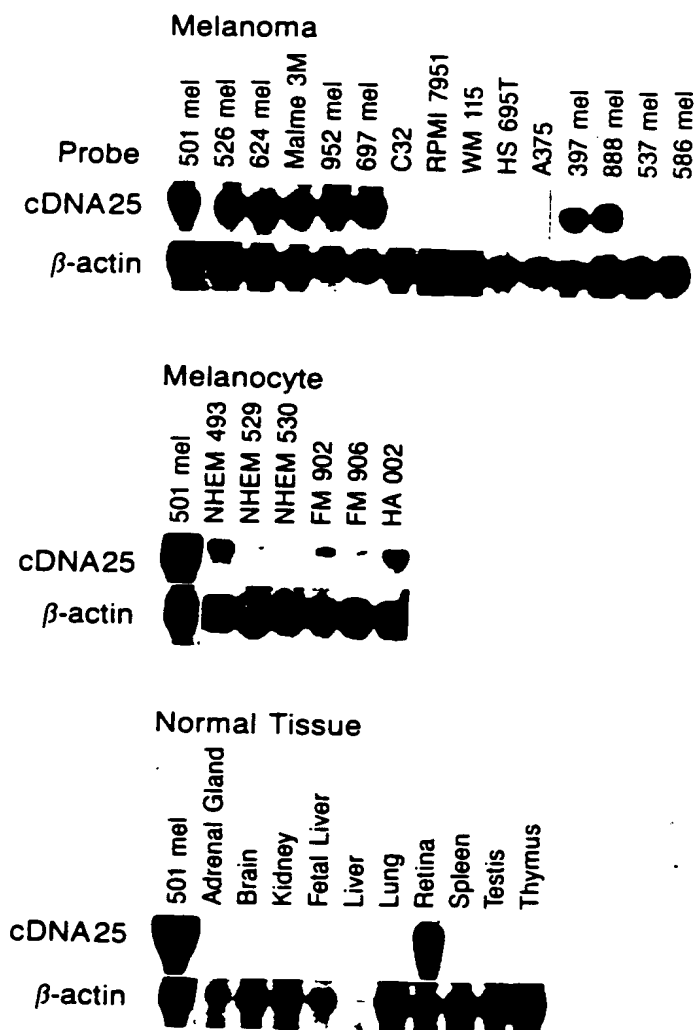


FIGURE 6